

STIC-Biotech/ChemLib

182078

mg

From: Chernyshev, Olga
Sent: Monday, March 13, 2006 4:47 PM
To: STIC-Biotech/ChemLib
Subject: 10/721,297, sequence search request

Please search SEQ ID NO: 1 and SEQ ID NO: 10 in regular databases only.
Thank you very much!

Olga N. Chernyshev, Ph.D.
AU 1649
REM 3C89
2-0870
mail 4C70

RECEIVED
MAR 14 2006
(STIC)

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2006, 20:08:12 ; Search time 146.5 Seconds
(without alignments)
33.711 Million cell updates/sec

Title: US-10-721-297-1

Perfect score: 34

Sequence: 1 EVKMDAB 7

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: UniProt_05.80.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	57	1 A4_URSMA	Q29149 u alzheimer
2	34	100.0	58	1 A4_CANFA	Q28280 c alzheimer
3	34	100.0	58	1 A4_RABIT	Q28748 o alzheimer
4	34	100.0	58	1 A4_SHEEP	Q28757 o alzheimer
5	34	100.0	59	1 A4_BOVIN	Q28053 b alzheimer
6	34	100.0	79	2 O35463_CRIGR	Q35463 cricetus
7	34	100.0	113	2 O8JH58_CHESE	Q8JH58 chelydra se
8	34	100.0	218	2 O8BPV5_MOUSE	O8BPV5 mus musculu
9	34	100.0	384	2 O8BPC7_MOUSE	O8BPC7 mus musculu
10	34	100.0	534	2 O93296_CHICK	O93296 gallus galli
11	34	100.0	569	2 O9PVL1_CHICK	O9PVL1 gallus galli
12	34	100.0	695	2 O5R477_PONPY	O5R477 pongo pygma
13	34	100.0	695	2 O6RH29_CANFA	O6RH29 canis famli
14	34	100.0	695	2 O56JK3_CANFA	O56JK3 canis famli
15	34	100.0	695	2 O6GR78_MOUSE	O6GR78 mus musculu
16	34	100.0	695	2 O9DGJ8_CHICK	O9DGJ8 gallus galli
17	34	100.0	714	2 O56JK4_CANFA	O56JK4 canis famli
18	34	100.0	733	2 O6P6Q5_RAT	O6P6Q5 rattus norv
19	34	100.0	749	2 O56JK2_STECO	O56JK2 sterculia co
20	34	100.0	751	1 A4_SALISC	O95241 s amyloid b
21	34	100.0	751	2 O6GSC0_HUMAN	O6GSC0 homo sapien
22	34	100.0	751	2 O6RH28_CANFA	O6RH28 canis famli
23	34	100.0	751	2 O56JK5_CANFA	O56JK5 canis famli
24	34	100.0	751	2 O4R4R8_MACFA	O4R4R8 macaca fasc
25	34	100.0	751	2 O9DGJ7_CHICK	O9DGJ7 gallus galli
26	34	100.0	770	1 A4_CAVPO	O60495 c amyloid b
27	34	100.0	770	1 A4_HUMAN	P05067 h amyloid b
28	34	100.0	770	1 A4_MACFA	P33601 m amyloid b
29	34	100.0	770	1 A4_MOUSE	P12023 m amyloid b
30	34	100.0	770	1 A4_PANTR	O51880 p amyloid b
31	34	100.0	770	1 A4_PIG	P79307 s amyloid b

32	34	100.0	770	1 A4_RAT	P08592 r amyloid b
33	34	100.0	770	2 O6RH30_CANFA	O6RH30 canis famli
34	34	100.0	770	2 O4SK76_CANFA	O4SK76 canis famli
35	34	100.0	770	2 O53ZT3_MOUSE	O53ZT3 mus musculu
36	34	100.0	770	2 O547B7_RAT	O547B7 rattus norv
37	31	91.2	119	2 O8ZFP0_PYRAE	O8ZFP0 pyrodictum
38	31	91.2	336	2 O6PC00_BRARE	O6PC00 brachydantio
39	31	91.2	354	2 O4SK78_TETRAO	O4SK78 tetradon n
40	31	91.2	693	2 O98SG0_XENLA	O98SG0 xenopus lae
41	31	91.2	695	2 O98SF9_XENLA	O98SF9 xenopus lae
42	31	91.2	695	2 O7ZXQ0_XENLA	O7ZXQ0 xenopus lae
43	31	91.2	747	2 O91963_XPIPI	O91963 xenopus ap
44	31	91.2	749	2 O6NR11_XENLA	O6NR11 xenopus lae
45	31	91.2	750	2 O6DJ66_XENTR	O6DJ66 xenopus tro

ALIGNMENTS

RESULT 1	A4_URSMA	STANDARD:	PRT:	57 AA.
AC	Q29149;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	10-MAY-2005 (Rel. 47, Last annotation update)			
DE	Alzheimer's disease amyloid A4 protein homolog [contains: Soluble APP-beta (S-APP-beta), CTF-alpha, Beta-amyloid protein 42 (Beta-APP42);			
DE	Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase			
DE	C-terminal fragment 59) (Gamma-CTF(57) (Gamma-secretase C-terminal			
DE	fragment 57)] (Fragment).			
GN	Name=APP;			
OS	Ursus maritimus (Polar bear) (Thalassarcha maritimus).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Ursidae;			
OC	Ursus.			
OX	NCBI_TaxID=29073;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Brain;			
RX	MEUJINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;			
RA	Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;			
RT	"Conservation of the sequence of the Alzheimer's disease amyloid			
RT	peptide in dog, polar bear and five other mammals by cross-species			
RT	polymerase chain reaction analysis.";			
RL	Brain Res. Mol. Brain Res. 10:299-305(1991).			
CC	-1- FUNCTION: Functional neuronal receptor which couples to			
CC	intracellular signaling pathway through the GTP-binding protein			
CC	G(O) (By similarity).			
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-1- SIMILARITY: Belongs to the APP family.			
CC	-----			
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use as long as its content is in no way modified and this statement is not			
CC	removed.			
CC	-----			
DR	EMBL; X56128; CA39593.1; -; mRNA.			
DR	PIR; B60045; B60045.			
DR	HSSP; P08592; INMJ.			
DR	InterPro; IPR008155; A4_APP.			
DR	InterPro; IPR001255; Beta-APP.			
DR	PANTHER; PTHR10083; SFG; Beta-APP; 1.			
DR	Pfam; PF03494; Beta-APP; 1.			
DR	PRINTS; PR00204; BETAAMYLOID.			
DR	PROSITE; PS00319; A4_EXTRA; PARTIAL.			
DR	PROSITE; PS00320; A4_INTRA; PARTIAL.			
KM	Amyloid; Transmembrane.			
FT	CHAIN	<1	5	Soluble APP-beta (By similarity).
FT	CHAIN	6	>57	CTF-alpha (By similarity).
FT	CHAIN	6	47	Beta-amyloid protein 42 (By similarity).
FT	CHAIN	6	45	Beta-amyloid protein 40 (By similarity).
FT	CHAIN	6	45	FT

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FT CHAIN 46 >57 Gamma-CTF(59) (By similarity).
FT CHAIN 48 >57 Gamma-CTF(57) (By similarity).
FT TOPO_DOM <1 33 Extracellular (Potential).
FT TRANSMEM 34 57 Potential.
FT NON_TER 1 1
FT NON_TER 57 57
SQ SEQUENCE 57 AA; 6172 MW; 84209888BA82DFA CRC64;

Query Match 100.0%; Score 34; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAE 7
Db 2 EVKMDAE 8

RESULT 2
A4 CANFA STANDARD; PRT; 58 AA.
ID A4 CANFA
AC Q28280;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
C-terminal fragment 59) (Gamma-CTF(57) (Gamma-secretase C-terminal
fragment 57)) (Fragment).
DE Name=APP;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OK NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -! FUNCTION: Functional neuronal receptor which couples to
intracellular signaling pathway through the GTP-binding protein
G(O) (By similarity).
CC -! SUBCELLULAR LOCATION: Type I membrane protein.
CC -! SIMILARITY: Belongs to the APP family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC EMBL: X56129; CAA39590.1; -; mRNA.
CC HSPF: P08592; INMT.
DR Ensemble; ENSGAF0000008557; Canis familiaris.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PANTHER; PTHR10083:SF6; Beta-APP; 1.
DR PRINTS; PR00204; BETAMYLOID.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Amyloid; Transmembrane.
FT CHAIN <1 6 Soluble APP-beta (By similarity).
FT CHAIN 7 58 CTF-alpha (By similarity).
FT CHAIN 7 48 Beta-amyloid protein 42 (By similarity).
FT CHAIN 7 46 Beta-amyloid protein 40 (By similarity).
FT CHAIN 47 >58 Gamma-CTF(59) (By similarity).
FT CHAIN 49 >58 Gamma-CTF(57) (By similarity).

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FT TOPO_DOM <1 34 Extracellular (Potential).
FT TRANSMEM 35 58 Potential.
FT NON_TER 1 1
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6285 MW; 8469D48A2E12DFA CRC64;

Query Match 100.0%; Score 34; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAE 7
Db 3 EVKMDAE 9

RESULT 3
A4 RABIT STANDARD; PRT; 58 AA.
ID A4 RABIT
AC Q28748;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
C-terminal fragment 59) (Gamma-CTF(57) (Gamma-secretase C-terminal
fragment 57)) (Fragment).
DE Name=APP;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OK NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
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CC HSPF: P08592; INMT.
DR Ensemble; ENSGAF0000008557; Canis familiaris.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR PANTHER; PTHR10083:SF6; Beta-APP; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAMYLOID.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Amyloid; Transmembrane.
FT CHAIN <1 5 Soluble APP-beta (By similarity).
FT CHAIN 6 58 CTF-alpha (By similarity).
FT CHAIN 6 47 Beta-amyloid protein 42 (By similarity).
FT CHAIN 6 45 Beta-amyloid protein 40 (By similarity).
FT CHAIN 46 >58 Gamma-CTF(59) (By similarity).
FT CHAIN 48 >58 Gamma-CTF(57) (By similarity).
FT TOPO_DOM <1 33 Extracellular (Potential).
FT TRANSMEM 34 57 Potential.
FT TOPO_DOM 58 >58 Cytoplasmic (Potential).

```

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OM protein - protein search, using sw model

Run on: March 15, 2006, 20:07:46 ; Search time 135 Seconds
(without alignments)
22.763 Million cell updates/sec

Title: US-10-721-297-1

Perfect score: 34

Sequence: 1 EVKMDAE 7

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_21:*

1: geneseqp1980s:*

2: geneseqp1980s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003as:*

8: geneseqp2004s:*

9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	7	8	ADJ71532 N-termina
2	34	100.0	7	9	AEA23387 Human APP
3	34	100.0	8	3	AAV94772 Beta-secr
4	34	100.0	8	4	AAU07230 Human bet
5	34	100.0	8	4	AAE10660 Human Asp
6	34	100.0	8	4	AAE06902 Human amy
7	34	100.0	8	4	AAE02612 Human Asp
8	34	100.0	8	4	AAU06635 Synthetic
9	34	100.0	8	4	AAU06631 Beta secr
10	34	100.0	8	5	ABW78621 APP Swedi
11	34	100.0	8	8	ADJ71533 N-termina
12	34	100.0	8	8	ADJ71545 N-termina
13	34	100.0	8	8	ADJ94379 Human amy
14	34	100.0	8	8	ADJ94379 Human amy
15	34	100.0	8	8	ADJ94379 Human amy
16	34	100.0	8	8	ADJ94379 Human amy
17	34	100.0	8	8	ADJ94379 Human amy
18	34	100.0	8	8	ADJ94379 Human amy
19	34	100.0	8	8	ADJ94379 Human amy
20	34	100.0	8	8	ADJ94379 Human amy
21	34	100.0	8	8	ADJ94379 Human amy
22	34	100.0	8	8	ADJ94379 Human amy
23	34	100.0	8	8	ADJ94379 Human amy
24	34	100.0	8	8	ADJ94379 Human amy

25	34	100.0	9	8	ADJ71546
26	34	100.0	9	8	ADS18111
27	34	100.0	9	8	AEA35404
28	34	100.0	10	2	AAE23054
29	34	100.0	10	2	AAE23054
30	34	100.0	10	2	AAE23054
31	34	100.0	10	3	AAE23054
32	34	100.0	10	4	AAU07227
33	34	100.0	10	4	AAE10654
34	34	100.0	10	4	AAE06899
35	34	100.0	10	4	AAE46208
36	34	100.0	10	4	AAE46207
37	34	100.0	10	4	AAE46209
38	34	100.0	10	4	AAE46206
39	34	100.0	10	4	AAE46206
40	34	100.0	10	4	AAE02606
41	34	100.0	10	4	AAE02606
42	34	100.0	10	4	AAE02606
43	34	100.0	10	4	AAE02606
44	34	100.0	10	5	ABW06426
45	34	100.0	10	5	ABG78375

ALIGNMENTS

RESULT 1	ADJ71532	ADJ71532 standard; peptide; 7 AA.
AC	ADJ71532;	
DT	06-MAY-2004	(first entry)
DE	N-terminal APP peptide C-terminal fragment, SEQ ID 195.	
DE	N-terminal APP peptide C-terminal fragment, SEQ ID 195.	
KW	Noctropic; Neuroprotective; Vaccine; beta Amyloid;	
KW	amyloid precursor protein; APP; Alzheimer's disease.	
OS	Homo sapiens.	
PN	W02004013172-A2.	
PD	12-FEB-2004.	
PR	18-JUL-2003; 2003WO-EP007833.	
PR	24-JUL-2002; 2002EP-00447147.	
PR	06-AUG-2002; 2002US-0401497P.	
XX	(INNO-) INNOGENETICS NV.	
XX	Delacourte A, Sergeant N;	
XX	WPI; 2004-180423/17.	
PT	New beta-amyloid or amyloid precursor protein preparation, useful as a	
PT	prophylactic vaccine or a therapeutic for preventing or treating a	
PT	disease associated with beta-amyloid formation and/or aggregation, e.g.	
PT	Alzheimer's disease.	
PS	Claim 7; Page 66; 104pp; English.	
XX	The present invention relates to preparations (I) comprising a beta-	
XX	amyloid peptide variant or beta-amyloid N-terminal fragment, or N-	
XX	terminal amyloid precursor protein (APP) soluble fragment or C-terminal	
XX	fragment. The beta-amyloid or APP preparations are useful for	
XX	manufacturing a prophylactic vaccine or a therapeutic, or as a	
XX	prophylactic vaccine for the prevention, or as a therapeutic for the	
XX	treatment of a disease associated with beta-amyloid formation and/or	
XX	aggregation, such as Alzheimer's disease.	
XX	Sequence 7 AA;	
XX		

Query Match	100.0%;	Score 34;	DB 8;	Length 7;
Best Local Similarity	100.0%;	Pred. Nc. 2e+06;		
Matches	7;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;

Qy	1	EVKMDAE	7
Db	1	EVKMDAE	7

RESULT 2
AEA23387
ID AEA23387 standard; peptide; 7 AA.

AC	AEA23387;
XX	
DT	28-JUL-2005 (first entry)

XX Screening; beta-amyloid; amyloid precursor protein; neuroprotective
KW neurotropic; degeneration; neurological disease; beta-secretase.
KW

OS Homo sapiens.
XX
PN US2005112696-A1.

PD	26-MAY-2005.
XX	
PF	25-NOV-2003; 2003US-00721297.

25-NOV-2003; 2003US-00721297.
(UYTE-) UNIV TEXAS SOUTHWESTERN MEDICAL CENT DAL

aa Sudhof TC, Li Q;
PI
XX
DR WPT: 2005-403362/41.

PT	nuclear localization.
XX	
PS	Claim 2; Page 10; 20pp; English.

	the human APP
CC	XX
XX	Sequence 7 AA;
sq	

QY	1	EVKMDAE	7
Db	1	EVKMDAE	7

RESULT 3
AA94772
ID AA94772 standard; protein; 8 AA

XX	12-FEB-2001 (first entry)
DT	
XX	
DE	Beta-secretase substrate peptide SEQ ID 18

XX Beta-secretase; enzyme; amyloid plaque; Alzheimer's disease;
KM Down's syndrome; amyloid angiopathy; gene therapy; neuroprotective
KM

OS	Synthetic.
XX	
PN	WO200058479-A1.

PD	05-OCT-2000.
XX	
PF	23-MAR-2000; 2000WO-US007755.

PR 26-MAR-1999; 99US-00277229.
XX
PA (AMGE-) AMGEN INC.

PI	Citron M, Vassar RJ, Bennett BD,
XX	
DR	WPI; 2000-594643/56.

PT Isolated beta-secretase nucleic acids and encoded polypeptides, useful
PT for diagnosis and gene therapy of Alzheimer's disease.
XX
PS Example 10; Page 117; 145p; English.

This invention relates to 3 nucleotide sequences encoding beta-secretase proteins. Beta-secretase is an enzyme involved in the production of one of the components of amyloid plaques involved in Alzheimer's disease. The invention includes an expression vector comprising the nucleotide sequence, a host cell comprising the expression vector, and a process for producing the protein through culturing the transformed cells. Also included in the invention are a polypeptide derivative of the beta-secretase protein, a fusion protein comprising beta-secretase fused to a heterologous amino acid sequence, and a method for modulating the levels of beta-secretase polypeptide in a mammal comprising administering the polynucleotide sequence. Beta-secretase exhibits neuroprotective and neurotropic activity. The beta-secretase nucleotide sequence may be used to map locations of the beta-secretase gene and related genes on chromosomes and as hybridization probes in diagnostic assays to test for the presence of beta-secretase DNA or RNA, such as in Alzheimer's disease, Down's syndrome, and amyloid angiopathy. The nucleotide sequence may also be used as anti-sense inhibitors of beta-secretase expression, in gene therapy of Alzheimer's disease, and for the identification of compounds that modulate beta-secretase activity. Antibodies to the beta-secretase protein may be used for in vitro and in vivo diagnostic purposes to detect the presence of beta-secretase polypeptide in a body fluid or cell sample. The present sequence represents a beta-secretase substrate peptide.

Sequence 8 AA:

Query Match	100.0%;	Score 34;	DB 3;	Length 8;
Best Local Similarity	100.0%;	Pred. No. 2e+06;		
Matches	7;	Conservative 0;	Mismatches 0;	Indels 0;
			Gaps	0;

QY	1	EVKMDAE	7
Db	1	EVKMDAE	7

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RESULT 4
AAU07230
ID    AAU07230 standard; peptide; 8 AA

```

DT	24-OCT-2001 (first entry)
XX	Human beta-amyloid protein precursor, APP-beta secretase site peptide #3
DE	

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO 67
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Peptide
US-09-548-367D-67

Query Match 100.0%; Score 34; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAE 7
DB 1 EVKMDAE 7

RESULT 3
US-09-551-853D-67
Sequence 67, Application US/09551853D
Patent No. 6500667
GENERAL INFORMATION:
APPLICANT: GURNEY ET AL.
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
FILE REFERENCE: 29915/6280L
CURRENT FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: US 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO 67
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Peptide
US-09-551-853D-67

Query Match 100.0%; Score 34; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAE 7
DB 1 EVKMDAE 7

RESULT 4
US-09-416-901B-67
Sequence 67, Application US/09416901B
Patent No. 6699671
GENERAL INFORMATION:
APPLICANT: GURNEY ET AL.
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
FILE REFERENCE: 29915/6280A

CURRENT APPLICATION NUMBER: US/09/416,901B
CURRENT FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: US 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn version 3.1
SEQ ID NO 67
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic Peptide
US-09-416-901B-67

Query Match 100.0%; Score 34; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAE 7
DB 1 EVKMDAE 7

RESULT 5
US-09-548-376D-67
Sequence 67, Application US/09548376D
Patent No. 6706485
GENERAL INFORMATION:
APPLICANT: GURNEY ET AL.
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
FILE REFERENCE: 29915/6280F
CURRENT FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO 67
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthesized peptide
US-09-548-376D-67

Query Match 100.0%; Score 34; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAE 7
DB 1 EVKMDAE 7

RESULT 6
US-09-794-927A-67
Sequence 67, Application US/09794927A
Patent No. 6727074
GENERAL INFORMATION:

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2006, 20:17:57 ; Search time 33.5 Seconds
(without alignments)
17.276 Million cell updates/sec

Title: US-10-721-297-1

Perfect score: 34

Sequence: 1 EVKMDAE 7

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	34	100.0	8	2	US-09-548-372D-67
3	34	100.0	8	2	US-09-551-853D-67
4	34	100.0	8	2	US-09-416-901B-67
5	34	100.0	8	2	US-09-548-376D-67
6	34	100.0	8	2	US-09-794-927A-67
7	34	100.0	8	2	US-09-548-373D-67
8	34	100.0	8	2	US-09-795-847B-67
9	34	100.0	8	2	US-09-869-414-67
10	34	100.0	8	2	US-09-548-366F-67
11	34	100.0	8	2	US-09-548-368D-67
12	34	100.0	8	2	US-09-794-925A-67
13	34	100.0	8	2	US-09-668-314C-70
14	34	100.0	8	2	US-09-794-743-67
15	34	100.0	9	2	US-08-802-981-221
16	34	100.0	9	2	US-09-294-987-6
17	34	100.0	9	2	US-09-724-566A-82
18	34	100.0	9	2	US-09-471-669A-82
19	34	100.0	10	1	US-08-025-321C-1
20	34	100.0	10	2	US-09-548-372D-64
21	34	100.0	10	2	US-09-548-367D-64
22	34	100.0	10	2	US-09-551-853D-64
23	34	100.0	10	2	US-09-604-608-4
24	34	100.0	10	2	US-09-416-901B-64
25	34	100.0	10	2	US-09-548-376D-64
26	34	100.0	10	2	US-09-794-927A-64
27	34	100.0	10	2	US-09-548-373D-64

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29	34	100.0	10	2	US-09-724-961-3	Sequence 3, Appli
30	34	100.0	10	2	US-09-724-961-4	Sequence 4, Appli
31	34	100.0	10	2	US-09-724-961-5	Sequence 5, Appli
32	34	100.0	10	2	US-09-724-961-6	Sequence 6, Appli
33	34	100.0	10	2	US-09-580-018-2	Sequence 2, Appli
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41	34	100.0	10	2	US-09-869-414-64	Sequence 6, Appli
42	34	100.0	10	2	US-09-548-366F-64	Sequence 64, Appli
43	34	100.0	10	2	US-09-548-368D-64	Sequence 64, Appli
44	34	100.0	10	2	US-09-794-925A-64	Sequence 64, Appli
45	34	100.0	10	2	US-09-668-314C-64	Sequence 64, Appli

ALIGNMENTS

RESULT 1
US-09-548-372D-67
Sequence 67, Application US/09548372D
Patent No. 6420534
GENERAL INFORMATION:
APPLICANT: GURNEY ET AL.
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
FILE REFERENCE: 29915/62801
CURRENT APPLICATION NUMBER: US/09/548,372D
CURRENT FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO 67
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Peptide
US-09-548-372D-67
Query Match 100.0%; Score 34; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 EVKMDAE 7
1 EVKMDAE 7
RESULT 2
US-09-548-367D-67
Sequence 67, Application US/09548367D
Patent No. 6440698
GENERAL INFORMATION:
APPLICANT: GURNEY ET AL.
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
FILE REFERENCE: 29915/62801
CURRENT APPLICATION NUMBER: US/09/548,367D
CURRENT FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/155,493

PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 67
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-794-927-67

Query Match 100.0%; Score 34; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAE 7
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DB 1 EVKMDAE 7

RESULT 3
US-09-795-847-67
Sequence 67, Application US/09795847
Patent No. US20010018208A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Bienkowski, Michael J.
APPLICANT: Heinrichson, Robert L.
APPLICANT: Parodi, Luis A.
APPLICANT: Yan, Riqiang
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
TITLE OF INVENTION: USES
FILE REFERENCE: 28341/6280DE
CURRENT APPLICATION NUMBER: US/09/795,847
CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 09/416,901
PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 67
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-795-847-67

Query Match 100.0%; Score 34; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 EVKMDAE 7

RESULT 4
US-09-794-743-67
Sequence 67, Application US/09794743
Patent No. US20010021391A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Bienkowski, Michael J.
APPLICANT: Heinrichson, Robert L.
APPLICANT: Parodi, Luis A.
APPLICANT: Yan, Riqiang
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
TITLE OF INVENTION: USES
FILE REFERENCE: 28341/6280BC
CURRENT APPLICATION NUMBER: US/09/794,743
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: 09/416,901
PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 67
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-794-743-67

Query Match 100.0%; Score 34; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAE 7
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DB 1 EVKMDAE 7

RESULT 5
US-09-794-748-67
Sequence 67, Application US/09794748
Patent No. US20020037315A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Bienkowski, Michael J.
APPLICANT: Heinrichson, Robert L.
APPLICANT: Parodi, Luis A.
APPLICANT: Yan, Riqiang
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
TITLE OF INVENTION: USES
FILE REFERENCE: 28341/6280UL
CURRENT APPLICATION NUMBER: US/09/794,748
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: 09/416,901
PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: Patentin Ver. 2.0

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2006, 20:18:47 ; Search time 120 Seconds

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24.373 Million cell updates/sec

Title: US-10-721-297-1

Perfect score: 34

Sequence: 1 EVKMDAE 7

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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SUMMARIES

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5	34	100.0	8	3	US-09-794-748-67
6	34	100.0	8	3	US-09-794-925-67
7	34	100.0	8	3	US-09-681-442-67
8	34	100.0	8	3	US-09-869-414-67
9	34	100.0	8	4	US-10-427-208-52
10	34	100.0	8	4	US-10-652-927-67
11	34	100.0	8	4	US-10-652-830-67
12	34	100.0	8	4	US-10-652-045-67
13	34	100.0	8	5	US-10-476-935-67
14	34	100.0	8	5	US-10-477-076-67
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22	34	100.0	9	5	US-10-625-854-220
23	34	100.0	9	6	US-11-090-866-82
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29	34	100.0	10	3	US-09-795-847-64	Sequence 64, App1
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31	34	100.0	10	3	US-09-794-748-64	Sequence 64, App1
32	34	100.0	10	3	US-09-796-264-4	Sequence 4, App1
33	34	100.0	10	3	US-09-794-925-64	Sequence 64, App1
34	34	100.0	10	3	US-09-681-442-64	Sequence 64, App1
35	34	100.0	10	3	US-09-845-226-4	Sequence 4, App1
36	34	100.0	10	3	US-09-908-903A-4	Sequence 20, App1
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ALIGNMENTS

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RESULT 1
US-10-625-854-195
Sequence 195, Application US/10625854
Publication No. US20050175626A1
GENERAL INFORMATION:
APPLICANT: Delacourte, Andr
TITLE OF INVENTION: Prevention, treatment and diagnosis of diseases associated with
FILE REFERENCE: 11362.0039.NPUS01 (INNS039---)
CURRENT APPLICATION NUMBER: US/10/625,854
CURRENT FILING DATE: 2003-07-23
PRIOR APPLICATION NUMBER: European Patent Application No. 02447147.6
PRIOR FILING DATE: 2002-07-24
PRIOR APPLICATION NUMBER: 60/401,497
PRIOR FILING DATE: 2002-08-06
NUMBER OF SEQ ID NOS: 261
SOFTWARE: PatentIn version 3.2
SEQ ID NO 195
LENGTH: 7
TYPE: PRT
ORGANISM: homo sapiens
US-10-625-854-195

Query Match      100.0%; Score 34; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EVKMDAE 7
Db      1 EVKMDAE 7

RESULT 2
US-09-794-927-67
Sequence 67, Application US/09794927
Patent No. US20010016324A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Bienkowski, Michael J.
APPLICANT: Heinrichson, Robert L.
APPLICANT: Parodi, Luis A.
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
TITLE OF INVENTION: USES
FILE REFERENCE: 28341/6280FG
CURRENT APPLICATION NUMBER: US/09/794,927
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: 09/416,901

```

CC (I) has neuroprotective and nootropic activities, and can be used in gene
CC therapy. (I) can be used for producing preparations of homogeneously
CC processed BACE that may be used for e.g. studying or treating diseases
CC such as Alzheimer's disease or Down's syndrome. The human BACE1 gene is
CC located on chromosome 11, more specifically to 11q23.2-23.3. The present
CC sequence represents a human BACE1 autoproteolysis site amino acid
CC sequence, which is used in the exemplification of the present invention.
XX
SQ Sequence 7 AA:

Query Match 100.0%; Score 34; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVNLDAE 7
DB 1 EVNLDAE 7

RESULT 2
ID AEA23394 standard; peptide; 7 AA.
XX
AC AEA23394;
XX
DT 28-JUL-2005 (first entry)
XX
DE Human APP beta-secretase cleavage site mutant peptide #2.
XX
KM Screening; beta-amyloid; amyloid precursor protein; neuroprotective;
XX
KW nootropic; degeneration; neurological disease; beta-secretase; muten.
XX
OS Homo sapiens.
XX
OS Synthetic.
XX
PN US2005112696-A1.
XX
PD 26-MAY-2005.
XX
PF 25-NOV-2003; 2003US-00721297.
XX
PR 25-NOV-2003; 2003US-00721297.
XX
PA (UYTE-) UNIV TEXAS SOUTHWESTERN MEDICAL CENT DAL.
XX
PI Sudhof TC, Li Q;
XX
DR WPI; 2005-403362/41.
XX
PT Identifying agents modulating cleavage of amyloid beta-precursor protein
PT by beta-secretase, by contacting chimeric molecule comprising cleavage
PT site with beta-secretase in presence of modulating agent, measuring
PT nuclear localization.
XX
PS Claim 3; Page 10; 20pp; English.
XX
CC The present invention relates to a method of screening and identifying
CC agents that modulate cleavage of amyloid beta-precursor protein (APP) or
CC APP-like proteins such as APLP1 and APLP2 by a beta-secretase. The method
CC involves contacting a chimeric molecule comprising a transmembrane region
CC (TMR) with a gamma- or beta-secretase cleavage site and an APP C-
CC terminal cytoplasmic tail modified with beta-secretase in presence and
CC absence of a modulating agent and identifying cleavage by measuring
CC nuclear localization of C-terminal cytoplasmic tail. The invention is
CC useful in the treatment of Alzheimer's disease. The present sequence is
CC the human APP beta-secretase cleavage site peptide containing Swedish
CC mutation.
XX
SQ Sequence 7 AA:

Query Match 100.0%; Score 34; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVNLDAE 7
DB 1 EVNLDAE 7

RESULT 3
ID AEB09785 standard; peptide; 7 AA.
XX
AC AEB09785;
XX
DT 08-SEP-2005 (first entry)
XX
DE Autoproteolysis sequence for engineered BACE1, SEQ ID 21.
XX
KM Protein engineering; Beta secretase; amyloid precursor protein;
XX
KW Alzhemers disease; Down syndrome; neuroprotective; nootropic;
XX
KW autoproteolytic site.
XX
OS Homo sapiens.
XX
OS WO2005060384-A2.
XX
PN WO2005060384-A2.
XX
PD 07-JUL-2005.
XX
PF 07-JUL-2004; 2004WO-US021816.
XX
PR 02-DEC-2003; 2003US-00726967.
XX
PA (SUNE-) SUNEIS PHARM INC.
XX
PI Ballinger M, Randal ML;
XX
DR WPI; 2005-497666/50.
XX
PT New polypeptide having beta site amyloid precursor protein APP-cleaving
PT enzyme (BACE) activity, having a prodomain, and autoproteolysis site and
PT protease domain, for producing preparations of homogeneously processed
PT BACE.
XX
PS Claim 12; SEQ ID NO 21; 71pp; English.
XX
CC The invention relates to a polypeptide (I) comprising in order from N-
CC terminus to C-terminus, a prodomain (comprising at least six contiguous
CC amino acids of AEB09767), an autoproteolysis site and a protease domain
CC (comprising at least one amino acid sequence chosen from a sequence at
CC least 90% identical to residues 74-207, 241-361 or 389-446 of AEB09765),
CC where the polypeptide is capable of being cleaved at the autoproteolysis
CC site, to thus release a free protease domain that has beta site amyloid
CC precursor protein (APP)-cleaving enzyme (BACE, beta secretase) activity.
CC Also included are a nucleic acid sequence encoding the polypeptide, a
CC vector for expressing the polypeptide and a host cell expressing the
CC polypeptide. The polypeptide is useful for producing preparations of
CC homogeneously processed BACE, and for cleaving amyloid precursor protein
CC at its beta-secretase site, to liberate Abeta peptide, where the cerebral
CC deposition of Abeta peptide causes Alzheimer's disease and Down's
CC syndrome. The polypeptide comprises a prodomain, an engineered cleavage
CC site, and a protease domain. The polypeptide is properly folded and is
CC cleaved at the engineered cleavage site in vitro, to produce homogenous
CC preparations of purified protease having BACE activity. The present
CC sequence is an autoproteolytic cleavage site which may be engineered into
CC the polypeptide of the invention.
XX
SQ Sequence 7 AA:

Query Match 100.0%; Score 34; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVNLDAE 7
DB 1 EVNLDAE 7

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OM protein - protein search, using sw model

Run on: March 15, 2006, 20:07:46 ; Search time 135 Seconds
(without alignments)
22.783 Million cell updates/sec

Title: US-10-721-297-10

Sequence: 1 EVNLDAE 7

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: A_Geneseq_21:*
2: geneseqp19808:*
3: geneseqp19908:*
4: geneseqp20008:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20048:*
8: geneseqp20058:*
9: geneseqp20058:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	100.0	7	8 ADP83933	Adp83933 Human BAC
2	34	100.0	7	9 Aea23394	Aea23394 Human APP
3	34	100.0	7	9 AEB09785	Aeb09785 Autoprote
4	34	100.0	8	3 AAY94771	Aay94771 Beta-secr
5	34	100.0	8	4 AAE10661	Aae10661 Human asp
6	34	100.0	8	4 AAE02613	Aae02613 Human Asp
7	34	100.0	8	5 ABB78622	Abb78622 Human bet
8	34	100.0	8	6 ABR54159	Abt54159 Beta-secr
9	34	100.0	8	9 AEA23385	Aea23385 Human APP
10	34	100.0	9	2 AAM82081	Aam82081 Fluorogen
11	34	100.0	9	3 AAB07874	Aab07874 A peptide
12	34	100.0	9	3 AAB07894	Aab07894 Substrate
13	34	100.0	9	4 AAG73297	Aag73297 Protease
14	34	100.0	9	5 ABB06519	Abb06519 Beta-secr
15	34	100.0	9	5 ABB09003	Abb09003 Peptide #
16	34	100.0	9	5 ABU60429	Abu60429 Protease
17	34	100.0	9	5 ABU60441	Abu60441 Protease
18	34	100.0	9	5 AAE16663	Aae16663 Oligopept
19	34	100.0	9	5 AAU74837	Aau74837 Synthetic
20	34	100.0	9	5 ABB07598	Abb07598 Synthetic
21	34	100.0	9	5 AAM50897	Aam50897 Oligopept
22	34	100.0	9	6 ABP97975	Abp97975 Synthetic
23	34	100.0	9	6 ABP57515	Abp57515 Different
24	34	100.0	9	6 ABP57084	Abp57084 Synthetic

25	34	100.0	9	6 ABP71468	Abp71468 Beta-secr
26	34	100.0	9	6 AAO16449	Aao16449 Beta-secr
27	34	100.0	9	6 ABP71269	Abp71269 Oligopept
28	34	100.0	9	6 ABR44377	Abt44377 Oligondep
29	34	100.0	9	6 ABP58375	Abp58375 Beta-secr
30	34	100.0	9	6 AAO26801	Aao26801 Beta-secr
31	34	100.0	9	6 ABG75940	Abg75940 Synthetic
32	34	100.0	9	6 ABP71630	Abp71630 Beta-secr
33	34	100.0	9	6 AAE36000	Aae36000 APP subsc
34	34	100.0	9	6 ABR82372	Abt82372 Beta-secr
35	34	100.0	9	6 ABR56258	Abt56258 Amyloid P
36	34	100.0	9	6 ABR62018	Abt62018 Beta-secr
37	34	100.0	9	6 ABR61887	Abt61887 Beta-secr
38	34	100.0	9	7 ABR56195	Abt56195 Amyloid P
39	34	100.0	9	7 ADC29723	Adc29723 Synthetic
40	34	100.0	9	7 ADC26557	Adc26557 Beta-secr
41	34	100.0	9	7 ADC10532	Adc10532 Synthetic
42	34	100.0	9	7 ADD80769	Add80769 Synthetic
43	34	100.0	9	8 ADG91228	Adg91228 Synthetic
44	34	100.0	9	8 ADV47996	Adv47996 Human BAC
45	34	100.0	9	8 ADM16649	Adm16649 Oligopept

ALIGNMENTS

RESULT 1
ADP83933 standard; peptide; 7 AA.
ID ADP83933
AC ADP83933;
AC ADP83933;
DT 23-SEP-2004 (first entry)
XX
XX
DE Human BACE1 autoproteolysis site SEQ ID NO:59.
KW human; beta-site amyloid precursor protein cleaving enzyme 1;
KW beta-site APP cleaving enzyme 1; BACE1; BACE1 isoform A; prodomain;
KW engineered cleavage site; protease domain; neuroprotective; nootropic;
KW gene therapy; Alzheimer's disease; Down's syndrome.
XX
XX
OS Homo sapiens.
XX
PN WO2004056962-A2.
XX
PD 08-JUL-2004.
XX
PF 02-DEC-2003; 2003WO-US038314.
XX
XX 04-DEC-2002; 2002US-0430984P.
XX
PA (SUNE-) SUNESIS PHARM INC.
XX
PI Ballinger M;
XX
DR WPI; 2004-507703/48.
XX
PT New polypeptides for producing homogenously processed preparations of
PT beta site amyloid precursor protein-cleaving enzyme comprises a
PT prodomain, an engineered cleavage site and a protease domain.
XX
PS Claim 10; SEQ ID NO 59; 40p; English.
XX
CC The present invention describes a polypeptide (I) comprising in order
CC from the N-terminus to the C-terminus: (a) a prodomain comprising at
CC least 6 contiguous amino acids of the 16 amino acid sequence of SEQ ID
CC NO:3 (ADP83877), comprising residues 22-37 of SEQ ID NO:1 (ADP83876) which
CC is the longest isoform of human beta-site amyloid precursor protein (APP)
CC cleaving enzyme 1 (BACE1), isoform A); (b) an engineered cleavage site;
CC and (c) a protease domain. (I) is capable of being cleaved at the
CC engineered cleavage site, and so releases a free protease domain that has
CC BACE1 activity. Also described: (1) a nucleic acid sequence encoding (I);
CC (2) a vector for expression of (I); and (3) a host cell expressing (I).

```

RESULT 3
H86169
hypothetical protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: H86169
R:Thellogis, A.; Becker, J.R.; Palm, C.U.; Pederspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lurce, J.S.; Malt, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: H86169
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-672 <STO>
A:Cross-references: UNIPROT:Q9ZWB1; UNIPARC:UPI00000A0A6A; GB:AE005172; NID:G4204304; PI
C:Genetics:
A:Map position: 1

Query Match
Best Local Similarity 91.2%; Score 31; DB 2; Length 672;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 EVNLDAB 7
DB 538 EVNLDSE 544

RESULT 4
T18655
hypothetical protein B0035.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18655
R:White, S.
submitted to the EMBL Data Library, May 1996
A:Reference number: Z19002
A:Accession: T18655
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-126 <WIL>
A:Cross-references: UNIPROT:Q17435; UNIPARC:UPI0000131727; EMBL:Z73102; PTDN:CAA97410.1;
A:Experimental source: clone B0035
C:Genetics:
A:Gene: CESP:B0035..4
A:Map position: 4 73/3
A:Introns: 29/3; 73/3
C:Superfamily: Arabidopsis thaliana hypothetical protein P22013.29

Query Match
Best Local Similarity 88.2%; Score 30; DB 2; Length 126;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 EVNLDAB 7
DB 119 QINLDAB 125

RESULT 5
A72411
hypothetical protein - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: A72411
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Hart, D.H.; Hickey

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Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: A72411
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-278 <ARN>
A:Cross-references: UNIPROT:Q9WT10; UNIPARC:UPI00000C146F; GB:AE001701; GB:AE000512; NID
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM0163

Query Match
Best Local Similarity 88.2%; Score 30; DB 2; Length 278;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 EVNLDAB 7
DB 241 EVNLDVE 247

RESULT 6
C81672
serine hydroxymethyltransferase TC0716 [imported] - Chlamydia muridarum (strain N19g)
C:Species: Chlamydia muridarum, Chlamydia trachomatis Mopn
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: C81672
R:Read, T.D.; Brubam, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39.
A:Reference number: A81500; MUID:20150255; PMID:10684935
A:Accession: C81672
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-497 <TET>
A:Cross-references: UNIPROT:Q9PVM0; UNIPARC:UPI0000057A25; GB:AE002340; GB:AE002160; NIT
A:Experimental source: strain N19g (Mopn)
C:Genetics:
A:Gene: TC0716
C:Superfamily: serine/glycine hydroxymethyltransferase

Query Match
Best Local Similarity 88.2%; Score 30; DB 2; Length 497;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 EVNLDAB 7
DB 202 EVNLDTE 208

RESULT 7
H71516
glycine hydroxymethyltransferase (EC 2.1.2.1) - Chlamydia trachomatis (serotype D, strain
N1)
A:Alternate names: serine hydroxymethyltransferase
C:Species: Chlamydia trachomatis
C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
C:Accession: H71516
R:Stephens, R.S.; Kalman, S.; Lammel, C.U.; Fan, J.; Marathe, R.; Arevind, L.; Mitchell,
Science 282, 754-759, 1998
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trac
A:Reference number: A71570; MUID:99000809; PMID:9784136
A:Accession: H71516
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-497 <ARN>
A:Cross-references: UNIPROT:O84439; UNIPARC:UPI000012B85B; GB:AE001316; GB:AE001273; NID
A:Experimental source: serotype D, strain UW-3/Cx
C:Genetics:
A:Gene: gLVA
C:Superfamily: serine/glycine hydroxymethyltransferase

```

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OM protein - protein search, using sw model

Run on: March 15, 2006, 20:13:01 ; Search time 24 Seconds
(without alignments)
28.063 Million cell updates/sec

Title: US-10-721-297-10

Perfect score: 34
Sequence: 1 EVNLDAB 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	419	2	D42725
2	31	91.2	368	2	A28825
3	31	91.2	672	2	H86169
4	30	88.2	126	2	T18655
5	30	88.2	278	2	A72411
6	30	88.2	497	2	C81672
7	30	88.2	497	2	H71516
8	30	88.2	802	2	C90326
9	29	85.3	282	2	T26112
10	29	85.3	289	2	D69795
11	29	85.3	295	2	F83867
12	29	85.3	326	2	A83087
13	29	85.3	340	2	T35558
14	29	85.3	394	2	F69888
15	29	85.3	400	2	E95099
16	29	85.3	400	2	D97967
17	29	85.3	434	2	D88305
18	29	85.3	434	2	S72430
19	29	85.3	442	2	B82633
20	29	85.3	470	2	C75591
21	29	85.3	508	2	B96658
22	29	85.3	550	2	AD3494
23	29	85.3	619	1	JH0776
24	29	85.3	712	2	AB2776
25	29	85.3	712	2	H97555
26	29	85.3	743	2	D64062
27	29	85.3	929	2	T52517
28	29	85.3	1331	2	H82211
29	28	82.4	161	1	G64814

30	28	82.4	161	2	F85586	molycopterin bios
31	28	82.4	161	2	E90736	molycopdenum cofacto
32	28	82.4	197	2	S61047	hypothetical prote
33	28	82.4	201	2	B84412	hypothetical prote
34	28	82.4	353	2	A95998	probable sugar upt
35	28	82.4	418	2	S56369	hypothetical 44.8k
36	28	82.4	418	2	H86109	probable transport
37	28	82.4	418	2	B98269	probable transport
38	28	82.4	459	2	S76122	hypothetical prote
39	28	82.4	509	2	D64435	hypothetical prote
40	28	82.4	533	2	T31002	hypothetical prote
41	28	82.4	538	2	AG3295	phosphoglycerate d
42	28	82.4	596	1	H02JUL	hydrogenase (BC 1,
43	28	82.4	597	2	B82881	hypothetical prote
44	28	82.4	809	2	S67665	ubiquitin-specific
45	28	82.4	970	2	C84488	hypothetical prote

ALIGNMENTS

RESULT 1
D42725
nitrite hydratase region 3'-hypothetical protein P47K - Pseudomonas chlororaphis (strat)
C:Species: Pseudomonas chlororaphis
C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #ext_change 09-Jul-2004
C:Accession: D42725
J. Bacteriol. 173, 2465-2472, 1991
R. Nishiyama, M. J. Horinouchi, S. J. Kobayashi, M. J. Nagaawa, T. J. Yamada, H. J. Beppu, T.
A:Title: Cloning and characterization of genes responsible for metabolism of nitrite co
A:Reference number: A42725; MUID:91193202; PMID:2013568
A:Accession: D42725
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-419 <NIS>
A:Cross-references: UNIPROT:P31521; UNIPARC:UPI000013102A; GB:D90216; NID:9216850; PIDN
C:Superfamily: conserved hypothetical protein yclC

Query Match 100.0%; Score 34; DB 2; Length 419;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVNLDAB 7
DB 48 EVNLDAB 54
RESULT 2
A28825
keratin, type I nonepidermal - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #ext_change 09-Jul-2004
C:Accession: A28825
R. Laflamme, S. E. J. Jamrich, M. J. Richter, K. J. Sargent, T. D. J. Dawid, I. B.
Genes Dev. 2, 853-862, 1988
A:Title: Xenopus endo B is a keratin preferentially expressed in the embryonic notochor
A:Reference number: A28825; MUID:89092007; PMID:2463213
A:Accession: A28825
A:Molecule type: mRNA
A:Residues: 1-368 <LAF>
A:Cross-references: UNIPROT:P08802; UNIPARC:UPI000012DAEC; GB:Y00230; NID:G64863; PIDN
C:Genetics:
A:Start codon: GGT
C:Superfamily: cytoskeletal keratin
C:Keywords: coiled coil

Query Match 91.2%; Score 31; DB 2; Length 368;
Best Local Similarity 85.7%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVNLDAB 7
DB 219 QVNLDAE 225


```

DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Transcription factor protein.
GN Name=C1-ATF3;
OS Ciona intestinalis.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC Phlebobranchia; Clonidae; Ciona.
OK NCBI_TaxID=7719;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15269171; DOI=10.1242/dev.01270;
RA Imai K.S., Hino K., Yagi K., Satoh N., Satou Y.;
RT "Genomewide surveys of developmentally relevant genes in Ciona
RT intestinalis.";
RL Development 131:4047-4058(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=12736827; DOI=10.1007/s00427-003-0330-z;
RA Satou Y., Satoh N.;
RT "Genomewide surveys of developmentally relevant genes in Ciona
RT intestinalis.";
RL Dev. Genes Evol. 213:211-212(2003).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Satou Y.;
RT "Expressed genes in Ciona intestinalis.";
RL Submitted (Apr-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB210313; BAE06318.1; -; mRNA.
SQ SEQUENCE 273 AA; 31974 MW; 4DD5C47C49B77361 CRC64;

Query Match 97.1%; Score 33; DB 2; Length 273;
Best Local Similarity 85.7%; Pred. No. 67;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 EVNLDAB 7
DB 217 EINDAB 223

RESULT 3
O6N9S6_RHOA PRELIMINARY; PRT; 402 AA.
AC O6N9S6;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN Ordered locus names=RP1462;
OS Rhodospirillum rubrum palustris.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiales; Rhodospirillum rubrum.
OK NCBI_TaxID=1076;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CGA009 / ATCC BAA-98;
RX PubMed=14704707; DOI=10.1038/nbt923;
RA Laxer F.W., Chai P., Hauser L., Lamerdin J.E., Malfatti S., Do L.,
RA Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,
RA Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Peters C.,
RA Harrison F.H., Gibson J., Harwood C.S.;
RT "Complete genome sequence of the metabolically versatile
RT photosynthetic bacterium Rhodospirillum rubrum palustris.";
RL Nat. Biotechnol. 22:55-61(2004).
DR EMBL; BX572597; CAE26904.1; -; Genomic_DNA.
DR InterPro; IPR003495; COB_W.
DR InterPro; IPR011629; COB_W.
DR Pfam; PF02492; COB_W.
DR Pfam; PF07683; COB_W.
DR Complete proteome; Hypothetical protein.
SQ SEQUENCE 402 AA; 45220 MW; 6D5A4A8B18E7791B CRC64;

Query Match 94.1%; Score 32; DB 2; Length 402;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;

```

```

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 EVNLDAB 7
DB 44 EVNIDAB 50

RESULT 4
O8PYH8_METWA PRELIMINARY; PRT; 84 AA.
AC O8PYH8;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Conserved protein.
GN Ordered locus names=MM0884;
OS Methanosarcina mazei (Methanosarcina frisia).
OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OK NCBI_TaxID=2209;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Goel / G01 / ATCC BAA-199 / DSM 3647 / OCM 88;
RX MEDLINE=22120827; PubMed=12125824;
RA Deppeleier U., Johann A., Hartsch T., Merkl R., Schmitz R.A.,
RA Martinez-Arias R., Henne A., Wietzer A., Baumer S., Jacobi C.,
RA Bruggemann H., Lienard T., Christmann A., Boemcke M., Steckel S.,
RA Bhattacharya A., Lykilds A., Overbeek R., Klenk H.-P., Gunsilius R.P.,
RA Fritz H.-D., Gottschalk G.;
RT "The genome of Methanosarcina mazei: evidence for lateral gene
RT transfer between Bacteria and Archaea.";
RL J. Mol. Microbiol. Biotechnol. 4:453-461(2002).
DR EMBL; AE013314; AAM30580.1; -; Genomic_DNA.
SQ SEQUENCE 84 AA; 9519 MW; F78DECBDE67B266 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 84;
Best Local Similarity 71.4%; Pred. No. 55;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 EVNLDAB 7
DB 78 EINDAB 84

RESULT 5
O8TW2_METAC PRELIMINARY; PRT; 84 AA.
AC O8TW2;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Predicted protein.
GN Ordered locus names=MA4028;
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OK NCBI_TaxID=2214;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CGA / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=11932238; DOI=10.1101/gr.223902;
RA Galagan J.E., Nussbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA Fitzhugh W., Calvo S., Engels R., Smirnov S., Atwood D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., Deatellano K., Johnson R.,
RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grame D.A., Guse A.M.,
RA Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Unayam L.A., White O., White R.H., de Macario E.C.,
RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.T.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 15, 2006, 20:08:12 ; Search time 146.5 Seconds
(without alignments)
33.711 Million cell updates/sec

Title: US-10-721-297-10
Perfect score: 34
Sequence: 1 EVNLDAB 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	100.0	419	1 P47K_PSECL	P31521 pseudomonas
2	33	97.1	273	2 Q4H3V9_CIOIN	Q4H3V9 clona intes
3	32	94.1	402	2 Q6N9S6_RHOPA	Q6N9S6 rhodopsin
4	31	91.2	84	2 Q8PYH8_METMA	Q8PYH8 methanosa
5	31	91.2	84	2 Q8RTW2_METMA	Q8RTW2 methanosa
6	31	91.2	118	2 Q4RZ22_TETNG	Q4RZ22 tetradon n
7	31	91.2	221	2 Q82W17_NITETU	Q82W17 nitrosomona
8	31	91.2	226	2 Q8TP55_METAC	Q8TP55 methanosa
9	31	91.2	281	2 Q8A4M0_BACTN	Q8A4M0 bacteroides
10	31	91.2	368	1 K1C18_XENLA	P08802 xenopus lae
11	31	91.2	402	2 Q6FBU8_ACTAD	Q6FBU8 actinobact
12	31	91.2	408	2 Q5NG56_FRATY	Q5NG56 francisella
13	31	91.2	428	2 Q6INH6_XENLA	Q6INH6 xenopus lae
14	31	91.2	436	2 Q8AVI2_XENLA	Q8AVI2 xenopus lae
15	31	91.2	672	2 Q9ZWB1_ARATH	Q9ZWB1 arabidopsis
16	31	91.2	1154	2 Q6WEZ0_PARUV	Q6WEZ0 paracalamyd
17	31	91.2	1186	2 Q522M9_MAGGR	Q522M9 magnaporthe
18	30	88.2	54	2 Q8P193_STRP8	Q8P193 streptococc
19	30	88.2	126	1 PFD4_CABEL	Q17435 caenorhabdi
20	30	88.2	126	2 Q6ISQ9_CABER	Q6ISQ9 caenorhabdi
21	30	88.2	142	2 Q60ZK3_CABER	Q60ZK3 caenorhabdi
22	30	88.2	222	2 Q5RCM3_EMENT	Q5RCM3 aspergillus
23	30	88.2	278	2 Q5CBM4_9THEM	Q5CBM4 thermotoga
24	30	88.2	278	2 Q5CBK6_9THEM	Q5CBK6 thermotoga
25	30	88.2	278	2 Q5CB78_9THEM	Q5CB78 thermotoga
26	30	88.2	278	2 Q5WY10_9THEM	Q5WY10 thermotoga
27	30	88.2	294	1 PHO85_YARLI	Q6C7U8 yarrowia li
28	30	88.2	330	1 PHO85_DEBIA	Q6BY22 debrayomyce
29	30	88.2	372	1 Q5V641_HALMA	Q5V641 haloarcula
30	30	88.2	497	1 GLYA_CHLNU	Q9P2W0 chlamydia m
31	30	88.2	497	1 GLYA_CHLTR	Q84439 chlamydia t

32	30	88.2	802	2 Q97XQ7_SUTISO	Q97XQ7 sulfolobus
33	30	88.2	926	2 Q5AYZ4_EMENT	Q5AYZ4 aspergillus
34	30	88.2	982	2 Q7QXJ8_GIALA	Q7QXJ8 giardia lam
35	29	85.3	81	2 Q6LXG3_METMA	Q6LXG3 methanococ
36	29	85.3	89	2 Q4NF12_9MICC	Q4NF12 archaebacte
37	29	85.3	142	2 Q8R7Z1_THETN	Q8R7Z1 thermosact
38	29	85.3	165	2 Q5GU43_XANOR	Q5GU43 xanthomonas
39	29	85.3	173	2 Q87ZB6_PSESM	Q87ZB6 pseudomonas
40	29	85.3	202	2 Q6CHW2_YARLI	Q6CHW2 yarrowia li
41	29	85.3	212	2 Q4ZRM4_PSESY	Q4ZRM4 pseudomonas
42	29	85.3	241	2 Q5P619_AZOSE	Q5P619 azoarcus sp
43	29	85.3	242	2 Q649N4_9ARCH	Q649N4 uncultured
44	29	85.3	255	2 Q4QK92_HAEI8	Q4QK92 haemophilus
45	29	85.3	260	2 Q5E3T6_VIBF1	Q5E3T6 vibrio fisc

ALIGNMENTS

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RESULT 1
P47K_PSECL          STANDARD;          PRT;          419 AA.
ID   P47K_PSECL          331521;
AC   P31521;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   47 kDa protein (P47K).
OS   Pseudomonas chlororaphis (Pseudomonas aureofaciens).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OX   Pseudomonadaceae; Pseudomonas.
NC   NCBI_TaxID=333;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC   STRAIN=B23;
RX   MEDLINE=91193202; PubMed=2013568;
RA   Nishiyama M., Horinouchi S., Kobayashi M., Nagasawa T., Yamada H.,
RA   Bepko T.;
RT   "Cloning and characterization of genes responsible for metabolism of
RT   nitrile compounds from Pseudomonas chlororaphis B23.";
RL   J. Bacteriol. 173:2465-2472(1991).
CC   -!- FUNCTION: The presence of P47K is critical for the expression of
CC   the nitrile hydratase genes. May stabilize or activate the nitrile
CC   hydratase proteins.
CC   -----
CC   EMBL, D90216; BAA14247.1; -; Genomic_DNA.
CC   PIR, D42725; D42725.
CC   HSSP: P24203; INTJ.
DR   InterPro, IPR011629; COBW_C.
DR   InterPro, IPR003495; P47K_Cob_synth.
DR   Pfam, PF02492; COBW_1.
DR   Pfam, PF07683; COBW_C; 1.
SQ   SEQUENCE 419 AA; 4666 MW; FFS13800E27FF0C CRC64;
Query Match          100.0%; Score 34; DB 1; Length 419;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY   1 EVNLDAB 7
Db   48 EVNLDAB 54

RESULT 2
ID   Q4H3V9_CIOIN          PRELIMINARY;          PRT;          273 AA.
AC   Q4H3V9;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)

```

TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
NUMBER OF SEQUENCES: 231
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/802,981
FILING DATE: 20-FEB-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 016665-000300US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 219:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-802-981-219

Query Match 100.0%; Score 34; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVNLDAE 7
Db 2 EVNLDAE 8

RESULT 3
US-09-724-566A-52
Sequence 52, Application US/09724566A
Patent No. 6627739
GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Basl, Guritqbal
APPLICANT: Doane, Minh Tam
APPLICANT: Frigon, No. 6627739mand
APPLICANT: John, Varghese
APPLICANT: Power, Michael
APPLICANT: Sinha, Sukanto
APPLICANT: Tatsuno, Gwen
APPLICANT: Tung, Jay
APPLICANT: Wang, Shuwen
APPLICANT: McConlogue, Lisa
TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
FILE REFERENCE: 228-US-NEWC2
CURRENT APPLICATION NUMBER: US/09/724,566A
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 09/501,708
PRIOR FILING DATE: 2000-02-10
PRIOR APPLICATION NUMBER: 60/119,571
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/139,172
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 104
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 52

LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligopeptide substrate
US-09-724-566A-52

Query Match 100.0%; Score 34; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVNLDAE 7
Db 2 EVNLDAE 8

RESULT 4
US-09-724-566A-83
Sequence 83, Application US/09724566A
Patent No. 6627739
GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Basl, Guritqbal
APPLICANT: Doane, Minh Tam
APPLICANT: Frigon, No. 6627739mand
APPLICANT: John, Varghese
APPLICANT: Power, Michael
APPLICANT: Sinha, Sukanto
APPLICANT: Tatsuno, Gwen
APPLICANT: Tung, Jay
APPLICANT: Wang, Shuwen
APPLICANT: McConlogue, Lisa
TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
FILE REFERENCE: 228-US-NEWC2
CURRENT APPLICATION NUMBER: US/09/724,566A
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 09/501,708
PRIOR FILING DATE: 2000-02-10
PRIOR APPLICATION NUMBER: 60/119,571
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/139,172
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 104
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 83
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: APP fragment P5-P4'wt
US-09-724-566A-83

Query Match 100.0%; Score 34; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVNLDAE 7
Db 2 EVNLDAE 8

RESULT 5
US-09-471-669A-52
Sequence 52, Application US/09471669A
Patent No. 6830918
GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Basl, Guritqbal
APPLICANT: Doane, Minh Tam
APPLICANT: Frigon, No. 6830918mand
APPLICANT: John, Varghese
APPLICANT: Power, Michael

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 15, 2006, 20:17:57 ; Search time 33.5 Seconds
(without alignments)
17.276 Million cell updates/sec

Title: US-10-721-297-10

Perfect score: 34

Sequence: 1 EVNLDAE 7

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA: *
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2: /cgn2_6/prodata/1/1aa/6.COMB.pep: *
3: /cgn2_6/prodata/1/1aa/H.COMB.pep: *
4: /cgn2_6/prodata/1/1aa/PCITUS.COMB.pep: *
5: /cgn2_6/prodata/1/1aa/RE.COMB.pep: *
6: /cgn2_6/prodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	34	100.0	8	2	US-09-668-314C-71	Sequence 71, Appl
2	34	100.0	9	2	US-08-802-981-219	Sequence 219, Appl
3	34	100.0	9	2	US-09-724-566A-52	Sequence 52, Appl
4	34	100.0	9	2	US-09-724-566A-83	Sequence 83, Appl
5	34	100.0	9	2	US-09-471-669A-52	Sequence 52, Appl
6	34	100.0	9	2	US-09-471-669A-83	Sequence 83, Appl
7	34	100.0	9	2	US-09-895-843-8	Sequence 8, Appl1
8	34	100.0	9	2	US-10-192-424-8	Sequence 8, Appl1
9	34	100.0	9	2	US-10-171-343-8	Sequence 8, Appl1
10	34	100.0	9	2	US-10-337-075-8	Sequence 8, Appl1
11	34	100.0	10	1	US-08-659-984A-19	Sequence 19, Appl
12	34	100.0	10	1	US-08-660-531-19	Sequence 19, Appl
13	34	100.0	10	2	US-09-548-372D-63	Sequence 63, Appl
14	34	100.0	10	2	US-09-548-372D-63	Sequence 63, Appl
15	34	100.0	10	2	US-09-548-372D-63	Sequence 63, Appl
16	34	100.0	10	2	US-09-548-372D-63	Sequence 63, Appl
17	34	100.0	10	2	US-09-548-372D-63	Sequence 63, Appl
18	34	100.0	10	2	US-09-548-372D-63	Sequence 63, Appl
19	34	100.0	10	2	US-09-548-372D-63	Sequence 63, Appl
20	34	100.0	10	2	US-09-548-372D-63	Sequence 63, Appl
21	34	100.0	10	2	US-09-548-372D-63	Sequence 63, Appl
22	34	100.0	10	2	US-09-548-372D-63	Sequence 63, Appl
23	34	100.0	10	2	US-09-548-372D-63	Sequence 63, Appl
24	34	100.0	10	2	US-09-548-372D-63	Sequence 63, Appl
25	34	100.0	10	2	US-09-548-372D-63	Sequence 63, Appl
26	34	100.0	10	2	US-09-548-372D-63	Sequence 63, Appl
27	34	100.0	10	2	US-09-548-372D-63	Sequence 63, Appl

28	34	100.0	10	2	US-09-548-365-63	Sequence 63, Appl
29	34	100.0	10	2	US-09-794-743-63	Sequence 63, Appl
30	34	100.0	11	4	PCT-US94-07043A-3	Sequence 3, Appl1
31	34	100.0	12	2	US-09-895-843-1	Sequence 1, Appl1
32	34	100.0	13	2	US-10-192-424-1	Sequence 1, Appl1
33	34	100.0	13	2	US-10-171-343-1	Sequence 1, Appl1
34	34	100.0	13	2	US-10-337-075-1	Sequence 1, Appl1
35	34	100.0	20	2	US-09-747-287A-198	Sequence 198, Appl
36	34	100.0	20	2	US-09-394-019C-150	Sequence 150, Appl
37	34	100.0	20	2	US-09-394-019C-395	Sequence 395, Appl
38	34	100.0	21	1	US-08-659-984A-18	Sequence 18, Appl
39	34	100.0	21	2	US-08-659-984A-112	Sequence 112, Appl
40	34	100.0	21	2	US-08-660-531-18	Sequence 18, Appl
41	34	100.0	21	2	US-09-404-578-18	Sequence 18, Appl
42	34	100.0	21	2	US-09-747-287A-172	Sequence 172, Appl
43	34	100.0	21	2	US-09-747-287A-173	Sequence 173, Appl
44	34	100.0	21	2	US-09-394-019C-125	Sequence 125, Appl
45	34	100.0	21	2	US-09-394-019C-370	Sequence 370, Appl

ALIGNMENTS

```
RESULT 1
US-09-668-314C-71
; Sequence 71, Application US/09668314C
; Patent No. 6844148
; GENERAL INFORMATION:
; APPLICANT: Gurney, et al
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; FILE REFERENCE: 28341/6280NCP
; CURRENT APPLICATION NUMBER: US/09/668,314C
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 60/169,232
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-668-314C-71

Query Match          100.0%; Score 34; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EVNLDAE 7
Db      1 EVNLDAE 7

RESULT 2
US-08-802-981-219
; Sequence 219, Application US/08802981
; Patent No. 6037137
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly S.
; TITLE OF INVENTION: Compositions for the Detection of Enzyme
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PRIOR APPLICATION NUMBER: 60/292,591
PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: 60/316,115
PRIOR FILING DATE: 2001-08-30
NUMBER OF SEQ ID NOS: 264
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 257
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Beta-Secretase Cleavage Site
US-10-480-954-257

Query Match 100.0%; Score 34; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVNLDAE 7.
Db 1 EVNLDAE 7

RESULT 3
US-10-817-979-71
Sequence 71, Application US/10817979
Publication No. US20050196398A1
GENERAL INFORMATION:

APPLICANT: Guirey, et al
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
FILE REFERENCE: 29915/40065
CURRENT APPLICATION NUMBER: US/10/817,979
CURRENT FILING DATE: 2004-04-05
PRIOR APPLICATION NUMBER: US 09/668,314
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: US 60/169,232
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: US 09/416,901
PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: US 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 84
SOFTWARE: PatentIn version 3.1
SEQ ID NO 71
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide
US-10-817-979-71

Query Match 100.0%; Score 34; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVNLDAE 7
Db 1 EVNLDAE 7

RESULT 4
US-09-896-874-8
Sequence 8, Application US/09896874
Patent No. US20020016320A1
GENERAL INFORMATION:
APPLICANT: Fang, Lawrence Y.

APPLICANT: John, Varghese
TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
FILE REFERENCE: 13615, 40USU1
CURRENT APPLICATION NUMBER: US/09/896,874
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215,323
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-896-874-8

Query Match 100.0%; Score 34; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVNLDAE 7
Db 2 EVNLDAE 8

RESULT 5
US-09-816-876-4
Sequence 4, Application US/09816876
Publication No. US20020019403A1
GENERAL INFORMATION:
APPLICANT: Hom, Roy
APPLICANT: Mamo, Shumeye
APPLICANT: Tung, Jay
APPLICANT: Gallinas, Andrea
APPLICANT: Varghese, John
APPLICANT: Fang, Larry
TITLE OF INVENTION: Methods to Treat Alzheimer's Disease
FILE REFERENCE: 01-1736-D
CURRENT APPLICATION NUMBER: US/09/816,876
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/191,528
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4
LENGTH: 9
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: synthetic peptide
US-09-816-876-4

Query Match 100.0%; Score 34; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVNLDAE 7
Db 2 EVNLDAE 8

RESULT 6
US-09-896-139-8
Sequence 8, Application US/09896139
Patent No. US20020128255A1
GENERAL INFORMATION:
APPLICANT: Beck, James P.
APPLICANT: Fang, Lawrence Y.
APPLICANT: Freskos, John N.
APPLICANT: Gallinas, Andrea
APPLICANT: Hom, Roy
APPLICANT: Jagodzinski, Barbara

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2006, 20:18:47 ; Search time 120 Seconds
(without alignments)
24.373 Million cell updates/sec

Title: US-10-721-297-10

Sequence: 1 EVNLDAE 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	100.0	7	US-10-726-967A-59	Sequence 59, Appl
2	34	100.0	8	US-10-480-954-257	Sequence 257, App
3	34	100.0	5	US-10-817-979-71	Sequence 71, Appl
4	34	100.0	9	US-09-896-874-8	Sequence 8, Appl
5	34	100.0	9	US-09-816-876-4	Sequence 4, Appl
6	34	100.0	9	US-09-896-139-8	Sequence 8, Appl
7	34	100.0	9	US-09-895-843-8	Sequence 8, Appl
8	34	100.0	9	US-09-908-943A-113	Sequence 113, App
9	34	100.0	9	US-09-895-871-8	Sequence 8, Appl
10	34	100.0	9	US-09-874-350A-209	Sequence 209, App
11	34	100.0	9	US-10-192-625-8	Sequence 8, Appl
12	34	100.0	9	US-10-192-424-8	Sequence 8, Appl
13	34	100.0	9	US-10-183-126A-8	Sequence 8, Appl
14	34	100.0	9	US-10-171-343-8	Sequence 8, Appl
15	34	100.0	9	US-10-264-707-8	Sequence 8, Appl
16	34	100.0	9	US-10-066-319-4	Sequence 4, Appl
17	34	100.0	9	US-10-337-075-8	Sequence 8, Appl
18	34	100.0	9	US-10-160-777-8	Sequence 8, Appl
19	34	100.0	9	US-10-192-543-8	Sequence 8, Appl
20	34	100.0	9	US-10-299-739-8	Sequence 8, Appl
21	34	100.0	9	US-10-685-898-107	Sequence 107, App
22	34	100.0	9	US-10-658-959A-8	Sequence 8, Appl
23	34	100.0	9	US-10-801-487-113	Sequence 113, App
24	34	100.0	9	US-10-801-938-113	Sequence 113, App
25	34	100.0	9	US-10-801-509-113	Sequence 113, App
26	34	100.0	9	US-10-801-486-113	Sequence 113, App
27	34	100.0	9	US-10-621-311-1	Sequence 1, Appl

28	34	100.0	9	US-10-828-582-8	Sequence 8, Appl
29	34	100.0	9	US-10-801-493-113	Sequence 113, App
30	34	100.0	9	US-11-075-161-8	Sequence 8, Appl
31	34	100.0	9	US-11-090-866-52	Sequence 52, Appl
32	34	100.0	9	US-11-090-866-83	Sequence 83, Appl
33	34	100.0	9	US-11-089-918-52	Sequence 52, Appl
34	34	100.0	9	US-11-089-918-83	Sequence 83, Appl
35	34	100.0	9	US-11-076-161-8	Sequence 8, Appl
36	34	100.0	9	US-11-069-377-52	Sequence 52, Appl
37	34	100.0	9	US-11-069-377-83	Sequence 83, Appl
38	34	100.0	9	US-11-090-872-52	Sequence 52, Appl
39	34	100.0	9	US-11-090-872-83	Sequence 83, Appl
40	34	100.0	9	US-11-090-399-52	Sequence 52, Appl
41	34	100.0	9	US-11-090-399-83	Sequence 83, Appl
42	34	100.0	9	US-11-042-695-8	Sequence 8, Appl
43	34	100.0	9	US-11-075-294-10	Sequence 10, Appl
44	34	100.0	9	US-11-074-828-10	Sequence 10, Appl
45	34	100.0	9	US-11-075-312-10	Sequence 10, Appl

ALIGNMENTS

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RESULT 1
US-10-726-967A-59
; Sequence 59, Application US/10726967A
; Publication No. US20050074456A1
; GENERAL INFORMATION:
; APPLICANT: Ballinger, Marcus
; TITLE OR INVENTION: Constructs for Homogenously Processed Preparations of Beta Site
; FILE REFERENCE: 2004345-0021
; CURRENT APPLICATION NUMBER: US/10/726,967A
; CURRENT FILING DATE: 2003-12-02
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 59
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Engineered BACE1 autoproteolysis site
US-10-726-967A-59

Query Match          100.0%; Score 34; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0;

QY      1 EVNLDAE 7
Db      1 EVNLDAE 7

RESULT 2
US-10-480-954-257
; Sequence 257, Application US/10480954
; Publication No. US20050032190A1
; GENERAL INFORMATION:
; APPLICANT: Brady, Stephen F.
; APPLICANT: Bruce, James E.
; APPLICANT: Chen-Dodson, Elizabeth
; APPLICANT: Garsky, Victor
; APPLICANT: Li, Yuenang
; APPLICANT: Sardana, Mohinder
; APPLICANT: Shafer, Jules A.
; APPLICANT: Tang, Xiaoting
; TITLE OR INVENTION: BETA-SECRETASE SUBSTRATES AND USES
; FILE REFERENCE: 200865YP
; CURRENT APPLICATION NUMBER: US/10/480,954
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: PCT/US02/15590
; PRIOR FILING DATE: 2002-05-17

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; APPLICANT: NEITZ, R. JEFFREY
; TITLE OF INVENTION: SUBSTITUTED UREA AND CARBAMATE, PHENACYL-2-HYDROXY-3-DIAMINOMALKAN
; FILE REFERENCE: 09511.0005-00000
; CURRENT APPLICATION NUMBER: US/11/075,292
; PRIOR FILING DATE: 2005-03-09
; PRIOR APPLICATION NUMBER: 60/622,589
; PRIOR FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: 60/591,857
; PRIOR FILING DATE: 2004-07-29
; PRIOR APPLICATION NUMBER: 60/575,829
; PRIOR FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: 60/551,192
; PRIOR FILING DATE: 2004-03-09
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-11-075-292-10

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Query Match          100.0%; Score 34; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 EVNLDAE 7
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Db 2 EVNLDAE 8

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RESULT 3
US-11-090-520-8
; Sequence 8, Application US/11090520
; Publication No. US20050267199A1
; GENERAL INFORMATION:
; APPLICANT: Hom, Roy
; APPLICANT: Tucker, John
; APPLICANT: John, Varghese
; APPLICANT: Shah, Neerav
; TITLE OF INVENTION: 2-Amino- and 2-Thio- Substituted 1,3-Diaminopropanes
; FILE REFERENCE: 04-244-A
; CURRENT APPLICATION NUMBER: US/11/090,520
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: 60/556,461
; PRIOR FILING DATE: 2004-03-25
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; US-11-090-520-8

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Query Match          100.0%; Score 34; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 EVNLDAE 7
    |||||
Db 2 EVNLDAE 8

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RESULT 4
US-11-038-790-10
; Sequence 10, Application US/11038790
; Publication No. US20060014790A1
; GENERAL INFORMATION:

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; APPLICANT: JOHN, VARGHESE
; APPLICANT: HOM, ROY
; APPLICANT: SEALY, JENNIFER
; APPLICANT: AQUINO, JOSE
; APPLICANT: PROBST, GARY
; APPLICANT: TUNG, JAY
; APPLICANT: FANG, LAWRENCE
; TITLE OF INVENTION: METHODS OF TREATMENT OF AMYLOIDOSIS USING
; FILE REFERENCE: 09511.0004-00000
; CURRENT APPLICATION NUMBER: US/11/038,790
; CURRENT FILING DATE: 2005-01-21
; PRIOR APPLICATION NUMBER: 60/619,948
; PRIOR FILING DATE: 2004-10-20
; PRIOR APPLICATION NUMBER: 60/619,947
; PRIOR FILING DATE: 2004-10-20
; PRIOR APPLICATION NUMBER: 60/619,917
; PRIOR FILING DATE: 2004-10-20
; PRIOR APPLICATION NUMBER: 60/591,885
; PRIOR FILING DATE: 2004-07-29
; PRIOR APPLICATION NUMBER: 60/591,908
; PRIOR FILING DATE: 2004-07-29
; PRIOR APPLICATION NUMBER: 60/591,858
; PRIOR FILING DATE: 2004-07-29
; PRIOR APPLICATION NUMBER: 60/575,858
; PRIOR FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: 60/575,798
; PRIOR FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: 60/575,799
; PRIOR FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: 60/537,551
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-11-038-790-10

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Query Match          100.0%; Score 34; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 EVNLDAE 7
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Db 2 EVNLDAE 8

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RESULT 5
US-11-075-445-10
; Sequence 10, Application US/11075445
; Publication No. US20060014737A1
; GENERAL INFORMATION:
; APPLICANT: JOHN, VARGHESE
; APPLICANT: HOM, ROY
; APPLICANT: SEALY, JENNIFER
; APPLICANT: TUCKER, JOHN
; TITLE OF INVENTION: METHODS OF TREATMENT OF AMYLOIDOSIS USING BI-ARYL ASPARTYL PROTEI
; FILE REFERENCE: 09511.0006-00000
; CURRENT APPLICATION NUMBER: US/11/075,445
; CURRENT FILING DATE: 2005-03-09
; PRIOR APPLICATION NUMBER: 60/551,205
; PRIOR FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: 60/551,013
; PRIOR FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: 60/575,964
; PRIOR FILING DATE: 2004-06-02

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2006, 20:19:57 ; Search time 15 Seconds
(without alignments)
13.357 Million cell updates/sec

Title: US-10-721-297-10

Perfect score: 34

Sequence: 1 EYNLDAE 7

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Total number of hits satisfying chosen parameters: 169630

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	34	100.0	9	7	US-11-075-445-10
6	34	100.0	9	7	US-11-218-879-8
7	34	100.0	10	6	US-10-895-861-2
8	34	100.0	11	6	US-10-348-595-2
9	34	100.0	11	6	US-10-348-595-4
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11	34	100.0	13	7	US-11-090-520-1
12	34	100.0	13	7	US-11-038-790-3
13	34	100.0	13	7	US-11-075-445-3
14	34	100.0	13	7	US-11-218-879-1
15	34	100.0	23	6	US-10-348-595-7
16	34	100.0	30	7	US-11-075-292-11
17	34	100.0	30	7	US-11-090-520-9
18	34	100.0	30	7	US-11-038-790-11
19	34	100.0	30	7	US-11-075-445-11
20	34	100.0	30	7	US-11-218-879-9
21	34	100.0	33	7	US-11-075-292-8
22	34	100.0	33	7	US-11-090-520-6
23	34	100.0	33	7	US-11-038-790-8
24	34	100.0	33	7	US-11-075-445-8
25	34	100.0	33	7	US-11-218-879-6

26	34	100.0	34	7	US-11-075-292-6	Sequence 6, Appl1
27	34	100.0	34	7	US-11-090-520-4	Sequence 4, Appl1
28	34	100.0	34	7	US-11-038-790-6	Sequence 6, Appl1
29	34	100.0	34	7	US-11-075-445-6	Sequence 6, Appl1
30	34	100.0	34	7	US-11-218-879-4	Sequence 4, Appl1
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32	28	82.4	181	7	US-11-096-568A-15093	Sequence 15093, A
33	28	82.4	206	7	US-11-096-568A-15092	Sequence 15092, A
34	27	79.4	226	7	US-11-096-568A-4752	Sequence 4752, Ap
35	27	79.4	231	7	US-11-096-568A-15700	Sequence 15700, A
36	27	79.4	250	7	US-11-096-568A-32295	Sequence 32295, A
37	27	79.4	251	7	US-11-096-568A-4751	Sequence 4751, Ap
38	27	79.4	254	7	US-11-096-568A-15699	Sequence 15699, A
39	27	79.4	260	7	US-11-096-568A-29072	Sequence 29072, A
40	27	79.4	289	7	US-11-096-568A-11346	Sequence 11346, A
41	27	79.4	322	7	US-11-096-568A-11345	Sequence 11345, A
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43	26	76.5	11	6	US-10-348-595-1	Sequence 1, Appl1
44	26	76.5	11	6	US-10-348-595-3	Sequence 3, Appl1
45	26	76.5	13	7	US-11-075-292-4	Sequence 4, Appl1

ALIGNMENTS

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RESULT 1
US-10-895-861-21
; Sequence 21, Application US/10895861
; Publication No. US20060019368A1
; GENERAL INFORMATION:
; APPLICANT: BALLINGER, Marcus
; TITLE OF INVENTION: CONSTRUCTS FOR HOMOGENOUSLY PROCESSED
; FILE REFERENCE: 39750-0027US
; CURRENT APPLICATION NUMBER: US/10/895,861
; CURRENT FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: US 60/430,984
; PRIOR FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: US 10/726,967
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: PCT to be assigned
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 7
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-895-861-21

Query Match      100.0%; Score 34; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

QY      1 EYNLDAE 7
Db      1 EYNLDAE 7

RESULT 2
US-11-075-292-10
; Sequence 10, Application US/11075292
; Publication No. US20050261273A1
; GENERAL INFORMATION:
; APPLICANT: JOHN, VARGHESE
; APPLICANT: MAILLARD, MICHEL
; APPLICANT: TUCKER, JOHN
; APPLICANT: AQUINO, JOSE
; APPLICANT: HOW, ROY
; APPLICANT: TUNG, UAY
; APPLICANT: DRESSEN, DARREN
; APPLICANT: SHAH, NEERAV

```